

Figure 1

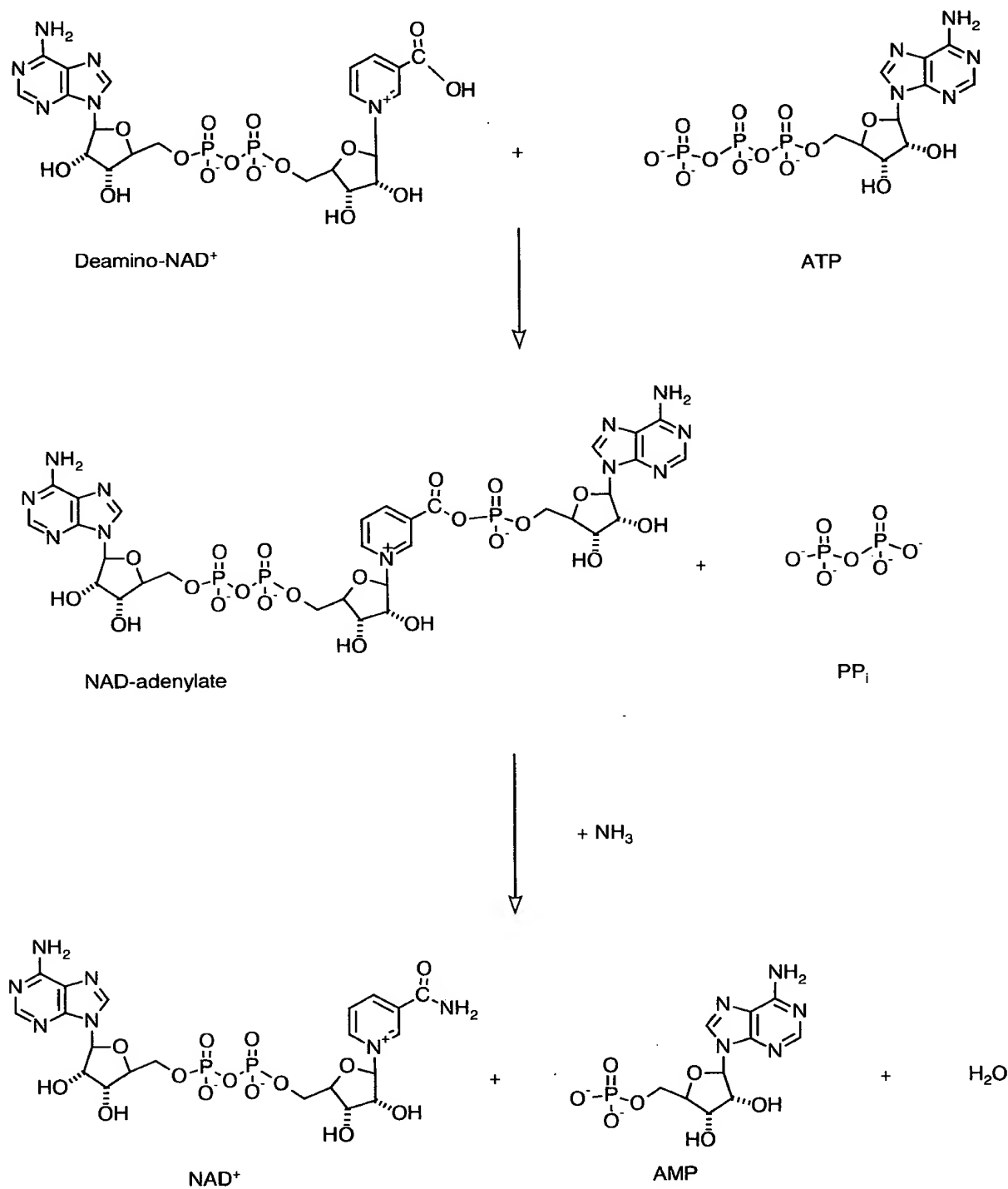
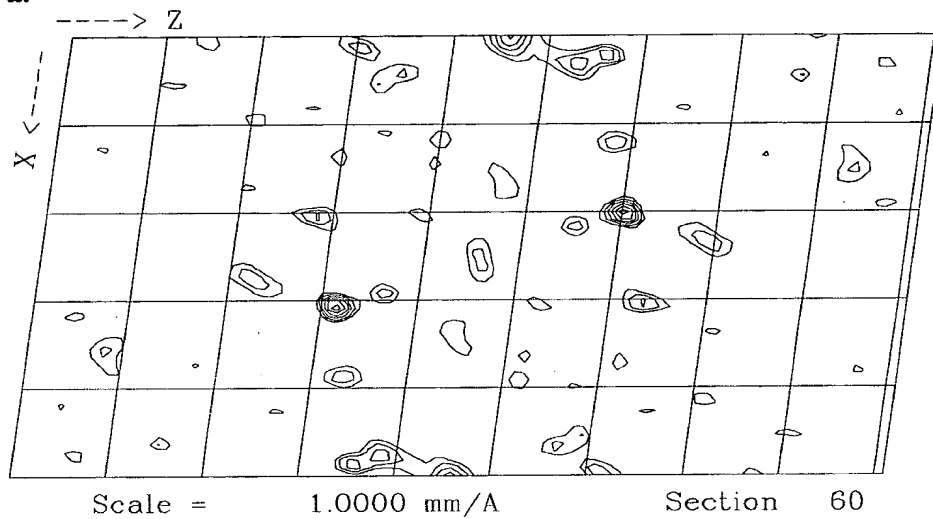


Figure 2

a.



b.

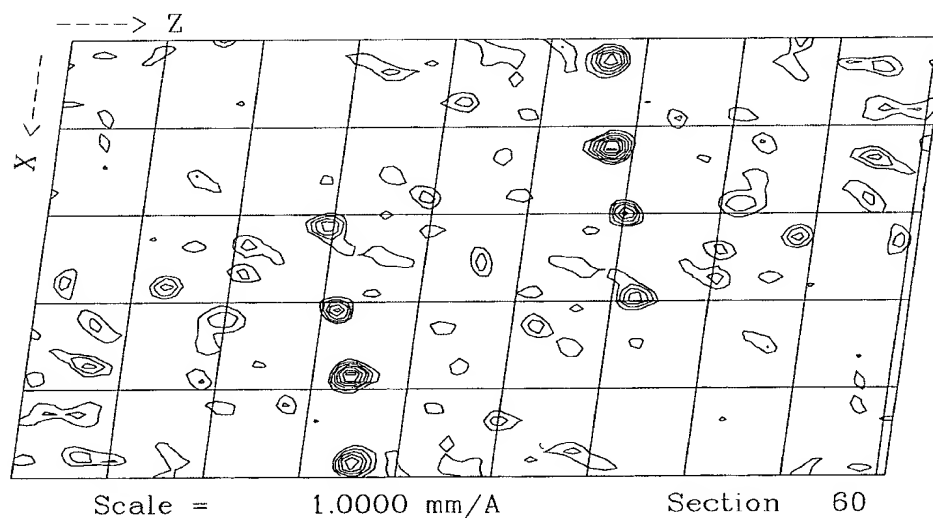
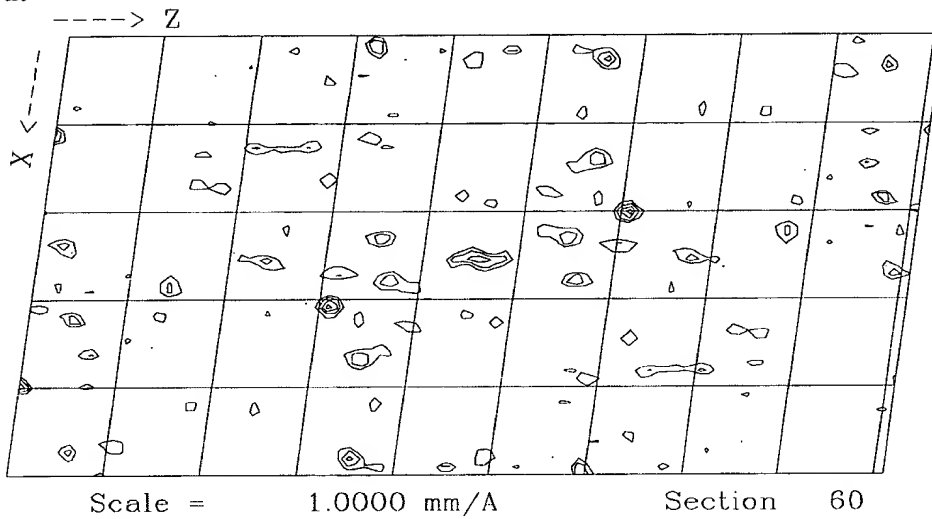


Figure 3

a.



b.

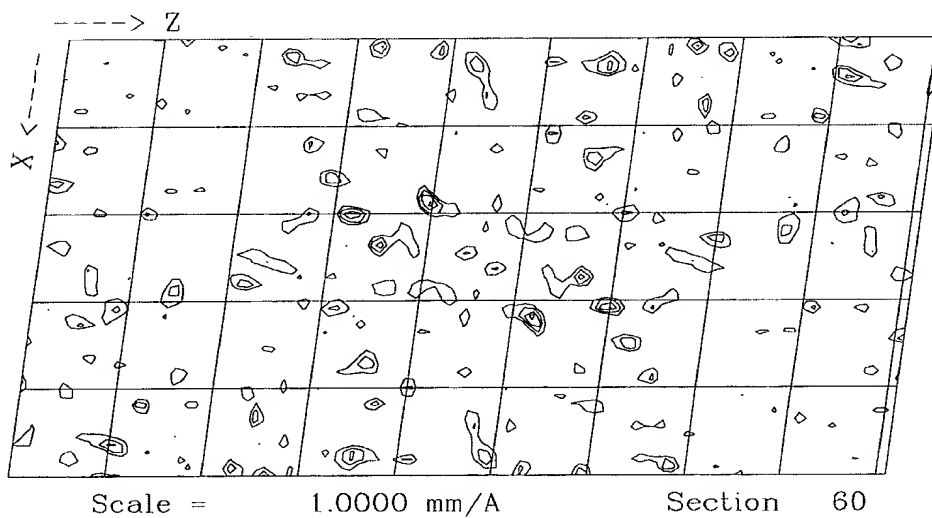
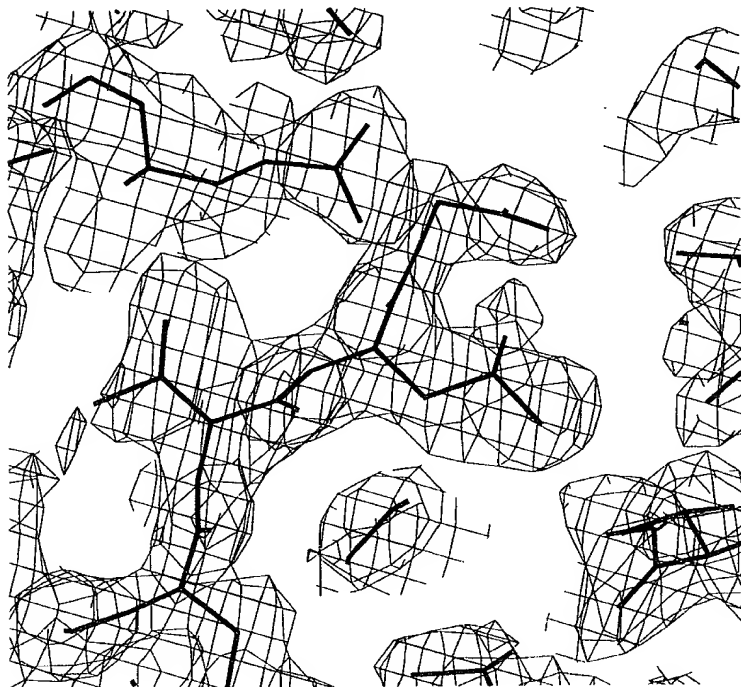


Figure 4

a.



b.

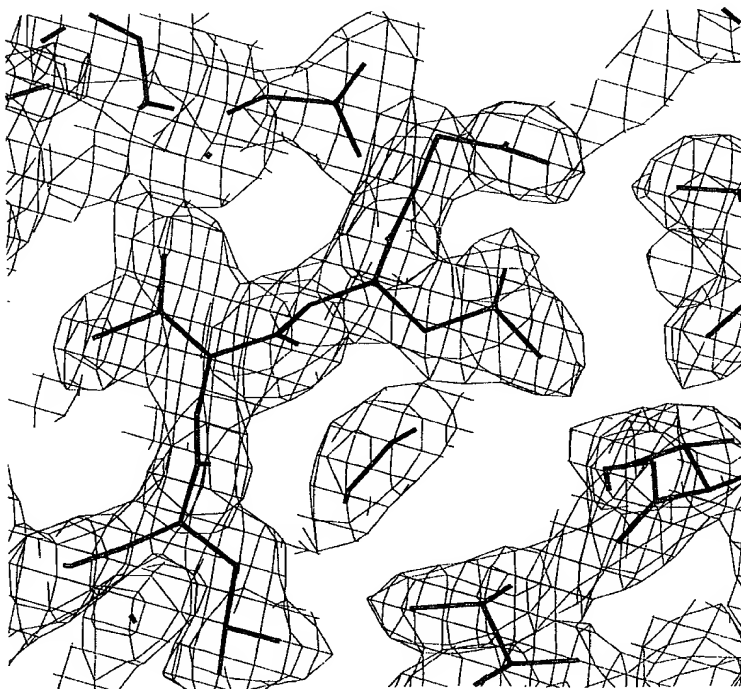


Figure 4a: 6315.N

Figure 5

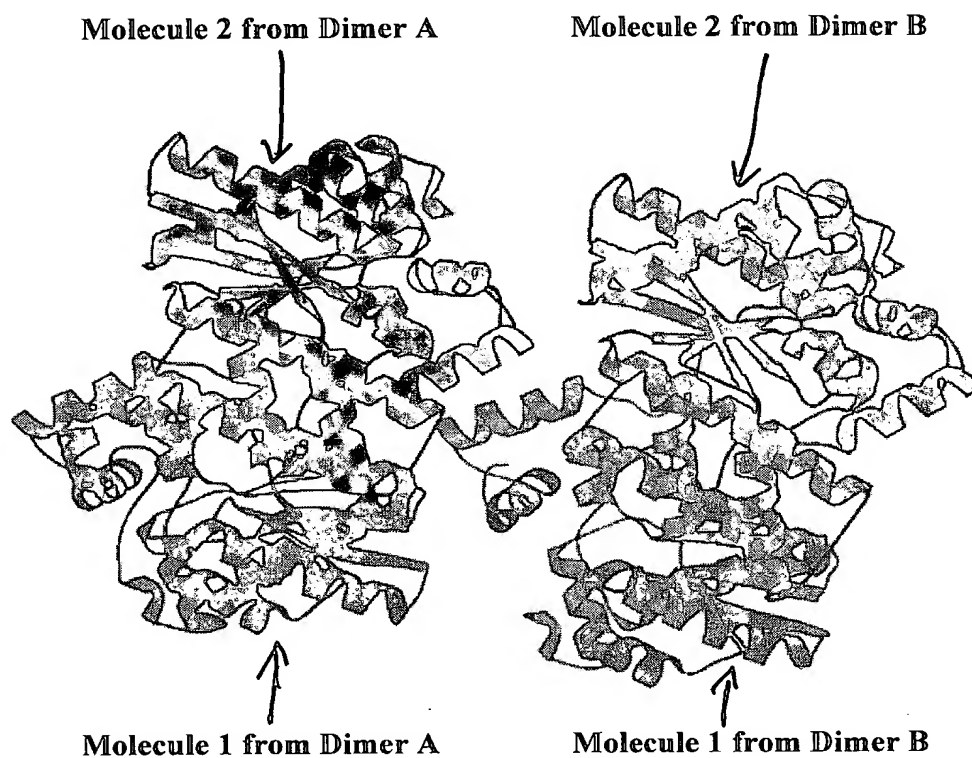


FIG. 5

Figure 6

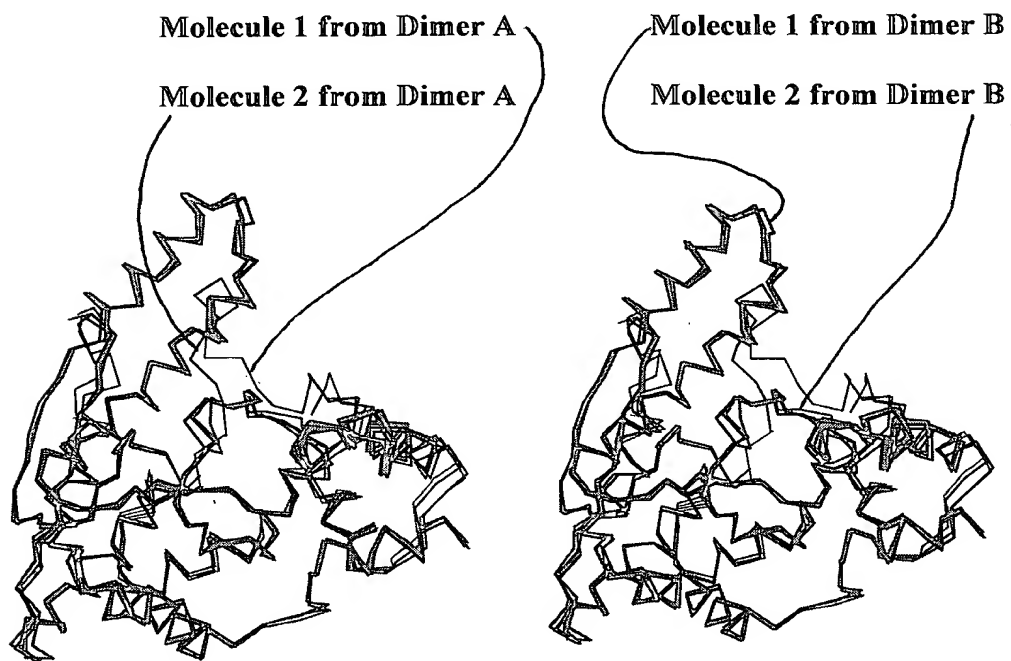
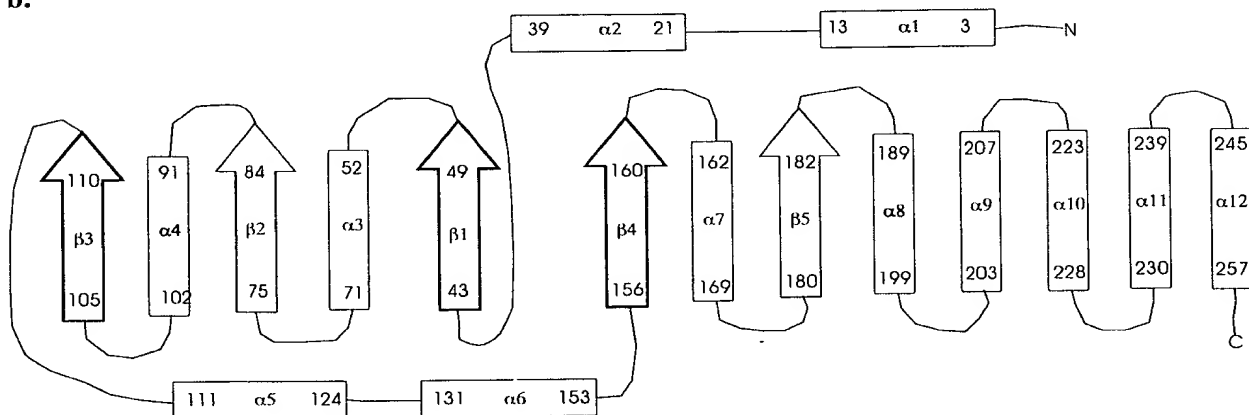


Figure 7

a.



b.



c.

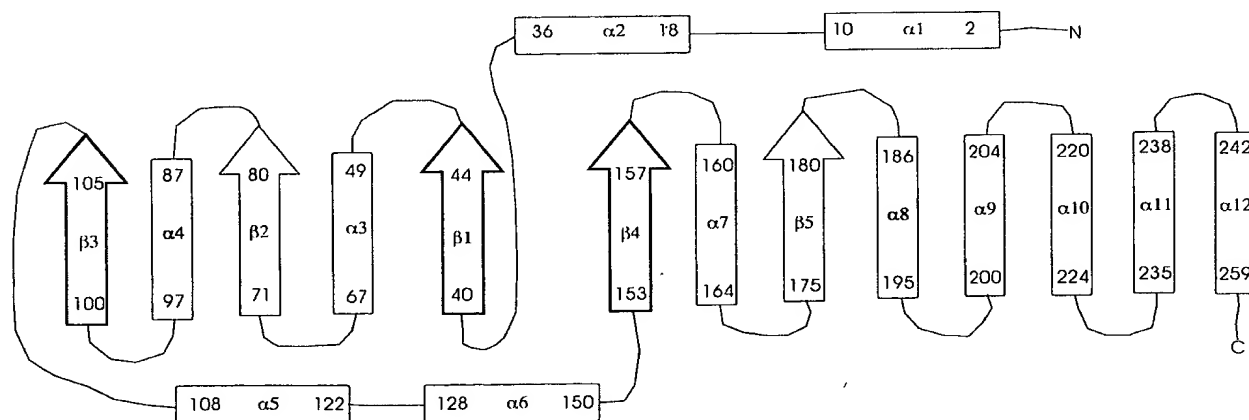


Figure 8



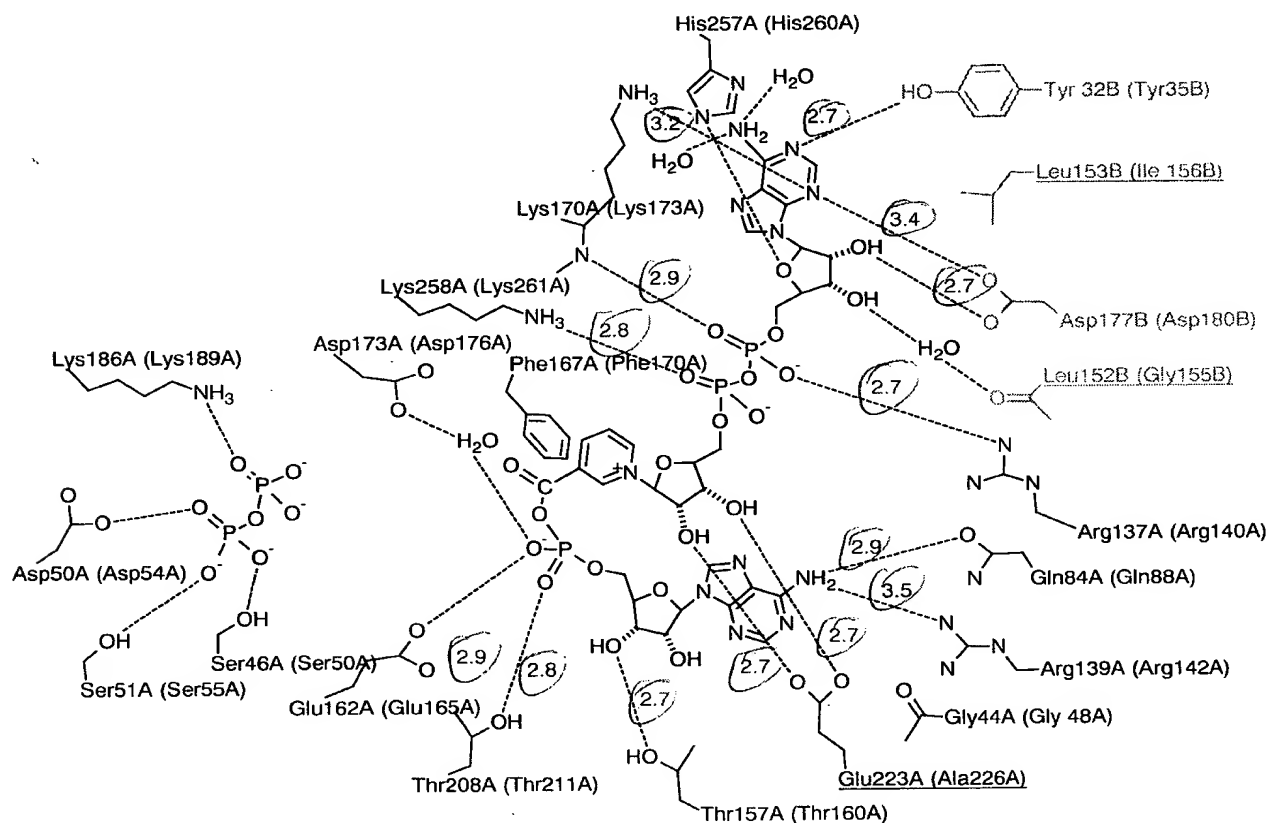
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Figure 9

		1		50
nade_bs	(1)	---	SMOEKIMRELHVKPSIDPKQEIERNFLKQYVK-KITGAKGFVLGIS	
nade_sa	(1)	MGSKLODVIMQEMVKKRIDSAAEIMELKQFIKKNYVQSHSFIKSLVLGIS		
		51		100
nade_bs	(47)	GGQDSTLAGRLAQFAVESIREEGGDAQFIAVRLPHGTQODEDDAQLALKEF		
nade_sa	(51)	GGQDSTLVGRLVQMSVNEIREEGIDCTFIAVKLPGVQKDADEVEQALRF		
		101		150
nade_bs	(97)	IKPKDSWKFDIKSTVSASFSDQYQOETGDQLTDFNKGNVKARTRMIAQYAI		
nade_sa	(101)	IEPDEIVTVNIKPAVDQS-VQSLKEAGIVLTDFOKGNEKARERMKVQESI		
		151		200
nade_bs	(147)	GGQEGLEVLGTDHAAEAVTGFFTKYGDGGADILPLTGLTKRQGRITLLKEL		
nade_sa	(150)	ASNRQGLVVGTDHSAENLTGFVTKYGDGAADTAPITFGLNKRQGRQLLAYL		
		201		250
nade_bs	(197)	GAPERLYLKEPTADLLDEKPOQSDTELGISYDEIDDYLEGKEVSAKVSE		
nade_sa	(200)	GAPKELYEKTPTADLEDDKPOLPDEDALGVITYDAIDNYLEGKPVITPEEQK		
		251		284
nade_bs	(247)	AEKRYSMTEHKRQMPASMEFDDWWK-----		
nade_sa	(250)	VLENHYIRNAHKRELAYRYT-WPKSRSHHHHHH		

[illegible]

Figure 10

[illegible]